

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101531,479
Source: PCT
Date Processed by STIC: 4-25-05

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/531,479

DATE: 04/25/2005
TIME: 12:24:32

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\04252005\J531479.raw

5 <110> APPLICANT: VIB vzw
9 <120> TITLE OF INVENTION: A role in lignification and growth for plant phenylcoumaran
benzylic

10 ether reductase
14 <130> FILE REFERENCE: WBO/PCBER/V130

C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/531,479

C--> 18 <141> CURRENT FILING DATE: 2005-04-15

18 <150> PRIOR APPLICATION NUMBER: EP 02079407.9

20 <151> PRIOR FILING DATE: 2002-10-18

24 <160> NUMBER OF SEQ ID NOS: 2

28 <170> SOFTWARE: PatentIn version 3.1

32 <210> SEQ ID NO: 1

34 <211> LENGTH: 1199

36 <212> TYPE: DNA

38 <213> ORGANISM: Populus balsamifera subsp. trichocarpa

42 <220> FEATURE:

44 <221> NAME/KEY: CDS

46 <222> LOCATION: (51)..(977)

48 <223> OTHER INFORMATION:

W--> 52 <400> 1

53	gcacgaggtt aaacttcctt ggtttcttc atcaagaaaa attatctaca atg gct	56
54		Met Ala
55		1
57	gat aaa agc aaa atc ttg atc att gga ggt act ggt tac ata gga aaa	104
58	Asp Lys Ser Lys Ile Leu Ile Ile Gly Gly Thr Gly Tyr Ile Gly Lys	
59	5 10 15	
61	ttc atc gtg gag gca agc gcc aag gcc ggt cac ccc act ttc gcc ttg	152
62	Phe Ile Val Glu Ala Ser Ala Lys Ala Gly His Pro Thr Phe Ala Leu	
63	20 25 30	
65	gtt aga gag agt aca gtc tct gat cct gtc aaa cga gaa ctt gtc gag	200
66	Val Arg Glu Ser Thr Val Ser Asp Pro Val Lys Arg Glu Leu Val Glu	
67	35 40 45 50	
69	aaa ttc aag aac tta ggc gtc act ttg atc cat gga gat gtc gac ggc	248
70	Lys Phe Lys Asn Leu Gly Val Thr Leu Ile His Gly Asp Val Asp Gly	
71	55 60 65	
73	cat gac aat ttg gtg aag gca atc aag cgg gtg gat gtg gtg ata tca	296
74	His Asp Asn Leu Val Lys Ala Ile Lys Arg Val Asp Val Ile Ser	
75	70 75 80	
77	gcg att ggg agc atg caa ata gca gat caa acc aag atc att gcc gcc	344
78	Ala Ile Gly Ser Met Gln Ile Ala Asp Gln Thr Lys Ile Ile Ala Ala	
79	85 90 95	
81	att aaa gaa gct ggc aat gtc aag aga ttc ttc cct tca gaa ttt gga	392.
82	Ile Lys Glu Ala Gly Asn Val Lys Arg Phe Phe Pro Ser Glu Phe Gly	
83	100 105 110	

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85 atg gat gtg gat cat gtc aat gct gtt gag cct gca aaa act gca ttt	440
86 Met Asp Val Asp His Val Asn Ala Val Glu Pro Ala Lys Thr Ala Phe	
87 115 120 125 130	
89 gca atg aag gct cag att cga cgt gcc atc gag gct gca ggg att ccc	488
90 Ala Met Lys Ala Gln Ile Arg Arg Ala Ile Glu Ala Ala Gly Ile Pro	
91 135 140 145	
93 tac act tat gtg cct tcc aac ttc ttt gct gca tat tat ctc ccc aca	536
94 Tyr Thr Tyr Val Pro Ser Asn Phe Phe Ala Ala Tyr Tyr Leu Pro Thr	
95 150 155 160	
97 ttg gca cag ttt gga ctt act gct cct ccg aga gac aag atc acc atc	584
98 Leu Ala Gln Phe Gly Leu Thr Ala Pro Pro Arg Asp Lys Ile Thr Ile	
99 165 170 175	
101 ctc gga gat ggc aat gcc aag ttg gtt ttc aat aag gaa gat gac att	632
102 Leu Gly Asp Gly Asn Ala Lys Leu Val Phe Asn Lys Glu Asp Asp Ile	
103 180 185 190	
105 gga acc tac acc atc aaa gct gtg gat gat gca aga acc ttg aac aag	680
106 Gly Thr Tyr Thr Ile Lys Ala Val Asp Asp Ala Arg Thr Leu Asn Lys	
107 195 200 205 210	
109 act gtc cta atc aag cct cct aaa aac acc tac tca ttc aat gag ctt	728
110 Thr Val Leu Ile Lys Pro Pro Lys Asn Thr Tyr Ser Phe Asn Glu Leu	
111 215 220 225	
113 att gat cta tgg gag aaa aag att ggc aaa acc ctc gaa aaa acc ttt	776
114 Ile Asp Leu Trp Glu Lys Lys Ile Gly Lys Thr Leu Glu Lys Thr Phe	
115 230 235 240	
117 gtt cct gaa gag aaa ctt ctg aag gac atc caa gag tct ccg att ccg	824
118 Val Pro Glu Glu Lys Leu Leu Lys Asp Ile Gln Glu Ser Pro Ile Pro	
119 245 250 255	
121 att aat att gtt ctg tca atc aac cac tca gcc ctc gtt aat ggt gac	872
122 Ile Asn Ile Val Leu Ser Ile Asn His Ser Ala Leu Val Asn Gly Asp	
123 260 265 270	
125 atg acc aac ttt gag att gac cca tca tgg ggc ctt gag gcc tct gag	920
126 Met Thr Asn Phe Glu Ile Asp Pro Ser Trp Gly Leu Glu Ala Ser Glu	
127 275 280 285 290	
129 cta tat cca gat gtc aaa tat acc acc gtg gaa gag tac ctt gat cag	968
130 Leu Tyr Pro Asp Val Lys Tyr Thr Thr Val Glu Glu Tyr Leu Asp Gln	
131 295 300 305	
133 ttt gtc tga ggcactggca ttcctgctc tccagttatt aatgaaacaa	1017
134 Phe Val	
137 acagccgaat agttggaaat ttgggtgtt cttataagacg agtgtttgtc caagtcaagg	1077
139 aggtctctt ccttataaac cttgtgaaat gatgttctgc tcttagttaat tgccatgggt	1137
141 tgtatctatt gctgaaagag atgttctggg tgagaataat gtaattgagt tatgatgaat	1197
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146 <210> SEQ ID NO: 2	
148 <211> LENGTH: 308	
150 <212> TYPE: PRT	
152 <213> ORGANISM: Populus balsamifera subsp. trichocarpa	
156 <400> SEQUENCE: 2	
158 Met Ala Asp Lys Ser Lys Ile Leu Ile Gly Gly Thr Gly Tyr Ile	
159 1 5 10 15	

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162 Gly Lys Phe Ile Val Glu Ala Ser Ala Lys Ala Gly His Pro Thr Phe
163 20 25 30
166 Ala Leu Val Arg Glu Ser Thr Val Ser Asp Pro Val Lys Arg Glu Leu
167 35 40 45
170 Val Glu Lys Phe Lys Asn Leu Gly Val Thr Leu Ile His Gly Asp Val
171 50 55 60
174 Asp Gly His Asp Asn Leu Val Lys Ala Ile Lys Arg Val Asp Val Val
175 65 70 75 80
178 Ile Ser Ala Ile Gly Ser Met Gln Ile Ala Asp Gln Thr Lys Ile Ile
179 85 90 95
182 Ala Ala Ile Lys Glu Ala Gly Asn Val Lys Arg Phe Phe Pro Ser Glu
183 100 105 110
186 Phe Gly Met Asp Val Asp His Val Asn Ala Val Glu Pro Ala Lys Thr
187 115 120 125
190 Ala Phe Ala Met Lys Ala Gln Ile Arg Arg Ala Ile Glu Ala Ala Gly
191 130 135 140
194 Ile Pro Tyr Thr Tyr Val Pro Ser Asn Phe Phe Ala Ala Tyr Tyr Leu
195 145 150 155 160
198 Pro Thr Leu Ala Gln Phe Gly Leu Thr Ala Pro Pro Arg Asp Lys Ile
199 165 170 175
202 Thr Ile Leu Gly Asp Gly Asn Ala Lys Leu Val Phe Asn Lys Glu Asp
203 180 185 190
206 Asp Ile Gly Thr Tyr Thr Ile Lys Ala Val Asp Asp Ala Arg Thr Leu
207 195 200 205
210 Asn Lys Thr Val Leu Ile Lys Pro Pro Lys Asn Thr Tyr Ser Phe Asn
211 210 215 220
214 Glu Leu Ile Asp Leu Trp Glu Lys Lys Ile Gly Lys Thr Leu Glu Lys
215 225 230 235 240
218 Thr Phe Val Pro Glu Glu Lys Leu Leu Lys Asp Ile Gln Glu Ser Pro
219 245 250 255
222 Ile Pro Ile Asn Ile Val Leu Ser Ile Asn His Ser Ala Leu Val Asn
223 260 265 270
226 Gly Asp Met Thr Asn Phe Glu Ile Asp Pro Ser Trp Gly Leu Glu Ala
227 275 280 285
230 Ser Glu Leu Tyr Pro Asp Val Lys Tyr Thr Thr Val Glu Glu Tyr Leu
231 290 295 300
234 Asp Gln Phe Val
235 305

VERIFICATION SUMMARY

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:52 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:48